```
                                         M   S   P   S   P   T   A   L   F   C   L
GGAGTCGACCCACGCGTCCGCAGGGCTGAGGAACC ATG TCT CCA TCC CCG ACC GCC CTC TTC TGT CTT     11
                                                                                     68

 G   L   C   L   G   R   V   P   A   Q   S   G   P   L   P   K   P   S   L   Q
GGG CTG TGT CTG GGG CGT GTG CCA GCG CAG AGT GGA CCG CTC CCC AAG CCC TCC CTC CAG      31
                                                                                     128

 A   L   P   S   S   L   V   P   L   E   K   P   V   T   L   R   C   Q   G   P
GCT CTG CCC AGC TCC CTG GTG CCC CTG GAG AAG CCA GTG ACC CTC CGG TGC CAG GGA CCT      51
                                                                                     188

 P   G   V   D   L   Y   R   L   E   K   L   S   S   S   R   Y   Q   D   Q   A
CCG GGC GTG GAC CTG TAC CGC CTG GAG AAG CTG AGT TCC AGC AGG TAC CAG GAT CAG GCA      71
                                                                                     248

 V   L   F   I   P   A   H   K   R   S   L   A   G   R   Y   R   C   S   Y   Q
GTC CTC TTC ATC CCG GCC ATG AAG AGA AGT CTG GCT GGA CGC TAC CGG TGC TCC TAC CAG      91
                                                                                     308

 N   G   S   L   W   S   L   P   S   D   Q   L   E   L   V   A   T   G   V   F
AAC GGA AGC CTC TGG TCC CTG CCC AGC GAC CAG CTG GAG CTC GTT GCC ACG GGA GTT TTT     111
                                                                                     368

 A   K   P   S   L   S   A   Q   P   G   P   A   V   S   S   G   G   D   V   T
GCC AAA CCC TCG CTC TCA GCC CAG CCC GGC CCG GCG GTG TCG TCA GGA GGG GAC GTA ACC     131
                                                                                     428

 L   Q   C   Q   T   R   Y   G   F   D   Q   F   A   L   Y   K   E   G   D   P
CTA CAG TGT CAG ACT CGG TAT GGC TTT GAC CAA TTT GCT CTG TAC AAG GAA GGG GAC CCT     151
                                                                                     488

 A   P   Y   K   N   P   E   R   W   Y   R   A   S   F   P   I   I   T   V   T
GCG CCC TAC AAG AAT CCC GAG AGA TGG TAC CGG GCT AGT TTC CCC ATC ATC ACG GTG ACC     171
                                                                                     548

 A   A   H   S   G   T   Y   R   C   Y   S   F   S   S   R   D   P   Y   L   W
GCC GCC CAC AGC GGA ACC TAC CGA TGC TAC AGC TTC TCC AGC AGG GAC CCA TAC CTG TGG     191
                                                                                     608

 S   A   P   S   D   P   L   E   L   V   V   T   G   T   S   V   T   P   S   R
TCG GCC CCC AGC GAC CCC CTG GAG CTT GTG GTC ACA GGA ACC TCT GTG ACC CCC AGC CGG     211
                                                                                     668

 L   P   T   E   P   P   S   S   V   A   E   F   S   E   A   T   A   E   L   T
TTA CCA ACA GAA CCA CCT TCC TCG GTA GCA GAA TTC TCA GAA GCC ACC GCT GAA CTG ACC     231
                                                                                     728

 V   S   F   T   N   K   V   F   T   T   E   T   S   R   S   I   T   T   S   P
GTC TCA TTC ACA AAC AAA GTC TTC ACA ACT GAG ACT TCT AGG AGT ATC ACC ACC AGT CCA     251
                                                                                     788

 K   E   S   D   S   P   A   G   P   A   R   Q   Y   Y   T   K   G   N   L   V
AAG GAG TCA GAC TCT CCA GCT GGT CCT GCC CGC CAG TAC TAC ACC AAG GGC AAC CTG GTC     271
                                                                                     848

 R   I   C   L   G   A   V   I   L   I   I   L   A   G   F   L   A   E   D   W
CGG ATA TGC CTC GGG GCT GTG ATC CTA ATA ATC CTG GCG GGG TTT CTG GCA GAG GAC TGG     291
                                                                                     908

 H   S   R   R   K   R   L   R   H   R   G   R   A   V   Q   R   P   L   P   P
CAC AGC CGG AGG AAG CGC CTG CGG CAC AGG GGC AGG GCT GTG CAG AGG CCG CTT CCG CCC     311
                                                                                     968

 L   P   P   L   P   Q   T   R   K   S   H   G   G   Q   D   G   G   R   Q   D
CTG CCG CCC CTC CCG CAG ACC CGG AAA TCA CAC GGG GGT CAG GAT GGA GGC CGA CAG GAT    1028

 V   H   S   R   G   L   C   S   *
GTT CAC AGC CGC GGG TTA TGT TCA TGA                                                  340
                                                                                    1055
```

FIGURE 1a

```
CCGCTGAACCCCAGGCACGGTCGTATCCAAGGGAGGGATCATGGCATGGGAGGCGACTCAAAGACTGGCGTGTGTGGAG   1136
CGTGGAAGCAGGAGGGCAGAGGCTACAGCTGTGGAAACGAGGCCATGCTGCCTCCTCCTGGTGTTCCATCAGGGAGCCG   1213
TTCGGCCAGTGTCTGTCTGTCTGTCTGCCTCTCTGTCTGAGGGCACCCTCCATTTGGGATGGAAGGAATCTGTGGAGAC   1292
CCCATCCTCCTCCCTGCACACTGTGGATGACATGGTACCCTGGCTGGACCACATACTGGCCTCTTTCTTCAACCTCTCT   1371
AATATGGGCTCCAGACGGATCTCTAAGGTTCCCAGCTCTCAGGGTTGACTCTGTTCCATCCTCTGTGCAAAATCCTCCT   1450
GTGCTTCCCTTTGGCCCTCTGTGCTCTTGTCTGGTTTTCCCCAGAAACTCTCACCCTCACTCCATCTCCCACTGCGGTC   1529
TAACAAATCTCCTTTCGTCTCTCAGAACGGGTCTTGCAGGCAGTTTGGGTATGTCATTCATTTTCCTTAGTGTAAAACT   1608
AGCACGTTGCCCGCTTCCCTTCACATTAGAAAACAAGATCAGCCTGTGCAACATGGTGAAACCTCATCTCTACCAACAA   1687
AACAAAAAAACACAAAAATTAGCCAGGTGTGGTGGTGCATCCCTATACTCCCAGCAACTCGGGGGGCTGAGGTGGGAGA   1766
ATGGCTTGAGCCTGGGAGGCAGAGGTTGCAGTGAGCTGAGATCACACCACTGCACTCTAGCTCGGGTGACGAAGCCTGA   1845
CCTTGTCTCAAAAAATACAGGGATGAATATGTCAATTACCCTGATTTGATCATAGCACGTTGTATACATGTACTGCAAT   1924
ATTGCTGTCCACCCCATAAATATGTACAATTATGTATACATTTTTAAAATCATAAAAATAAGATAATGAAAAAAAAAAA   2003
AAAAAAAAAAAAAAGGGCGGGCCGCTAGACTAGTCTAGAGAACA                                     2047
```

FIGURE 1b
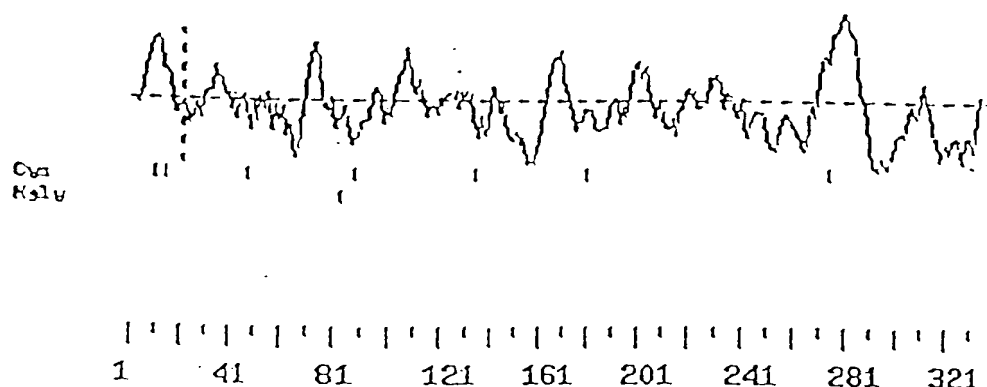
HSPSPTALFCLGLCLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGPPGVDLYRLE
KLSSSRYQDQAVLFIPAMKRSLAGRYRCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQP
GPAVSSGGDVTLQCQTRYGFDQFALYKEGDPAPYKNPERWYRASFPIITVTAAHSGTYRC
YSFSSRDPYLWSAPSDPLELVVTGTSVTPSRLPTEPPSSVAEFSEATAELTVSFTNKVFT
TETSRSITTSPKESDSPAGPARQYYTKGNLVRICLGAVILIILAGFLAEDWHSRRKRLRH
RGRAVQRPLPPLPPLPQTRKSHGGQDGGRQDVHSRGLCS

FIGURE 2

```
ALIGN calculates a global alignment of two sequences
  version 2.0uPlease cite: Myers and Miller, CABIOS (1989)
 > U91928 ORF                                    1893 aa vs.
 > hT268 ORF                                     1017 aa
scoring matrix: pam120.mat, gap penalties: -12/-4
37.7% identity;           Global alignment score: -8

              10        20        30        40        50        60        70
inputs ATGACGCCCGCCCTCACAGCCCTGCTCTGCCTTGGGCTGAGTCTGGGCCCCAGGACCCGCGTGCAGGCAG
       :::..: ::  :::   ::  :::::  ::::  :::::::::.::::::: :  .: .:: ::  ::::. .:
       ATGTCTCCATCCCCGACCGCCCTCTTCTGTCTTGGGCTGTGTCTGGGCG-TGTGCCAGC--GCAGAGTG
         10        20        30        40        50        60

              80        90       100       110       120       130
inputs GGCCCTTCCCCAAACCCACCCTCTGGGCTGAGCCAGGCTCTGTGAT-CAGCTGGGGGAGCCCCGTGACCA
       :.:: :::::::::.:::.::::: .:::: .::: .:::: ::.: : :::::.:.:::: :::::::
       GACCGCTCCCCAAGCCCTCCCTCCAGGCTCTGCCCAGCTCCCTGGTGCCCCTGGAGAAGCCA-GTGACCC
         70        80        90       100       110       120       130

            140       150       160       170       180       190       200
inputs TCTGGTGTCAGGGGAGCCTGGAGGCCCAGGAGTACCGACTGGATAAAGAGGGAAGCCCAGAGCCCTTGGA
       :: ::::: :::::  .:::       ::.:: ::. ::: ::.            ::: .:::       ...
       TCCGGTGCCAGGG--ACCT------CCGGGCGTG--GACCTGTA--------CCGCCTGGAG-----AAG
         140       150              160    .     170              180

            210      '220       230       240       250       260       270
inputs CAGAAATAACCCACTGGAACCCAAGAACAAGGCCAGATTCTCCATCCCATCCATGACAGAGCACCATGCG
       :.::..: :: .:.::.::: :.::.:: ::: .    ::: :::::::. :::::: ....  . :. ::
       CTGAGTT--CCAGCAGGTACC-AGGATCA-GGCAGTCCTCTTCATCCCGGCCATGAAGAGAAGTCTGGCT
         190         200       210       220       230       240

            280       290       300       310       320       330       340
inputs GGGAGATACCGCTGCCACTATTACAGCTCTGCAG--GCTGGTCAGAGCCCAGCGACCCCCTGGAGCTGGT
       ::. : :::::::::: :::   ::: .: : ::   :::::: .:::::::::: :::::::: ::
       GGACGCTACCGCTGCTCCTAC--CAGAACGGAAGCCTCTGGTCCCTGCCCAGCGACCAGCTGGAGCTCGT
         250       260       270       280       290       300       310

            350       360       370       380       390       400       410
inputs GATGACAGGATTCTACAACAAACCCACCCTCTCAGCCCTGCCCAGCCCTGTGGTGGCCTCAGGGGGGAAT
       .  ::.::: : :. . :::::::.: ::::::::::::.::::.:::: : :::: : :::::.:::.:
       TGCCACGGGAGTTTTTGCCAAACCCTCGCTCTCAGCCCAGCCCGGCCCGGCGGTGTCGTCAGGAGGGGAC
         320       330       340       350       360       370       380

            420       430       440       450       460       470       480
inputs ATGACCCTCCGATGTGGCTCACAGAAGGGATATCACCATTTTGTTCTGATGAAGGAAGGAGAACACCAGC
       .:.::::: :..::: . .:.:.:.: :: :: ::::.::: :::::.. :::::::::
       GTAACCCTACAGTGTCAGACTCGGTATGGCTTTGACCAATTTGCTCTGTACAAGGAAGG-----------
         390       400       410       420       430       440

            490     .  500       510       520       530       540       550
inputs TCCCCCGGACCCTGGACTCACAGCAGCTCCACAGTGGGGGGGTTCCAGGCCCTGTTCCCTGTGGGCCCCGT
       ::::::::                                   :  :::::.            :..
```

FIGURE 3a

```
      ------GGACCCTG---------------------------------C---GCCCTA--------------CAA
            450                                              460

         560       570       580       590       600       610       620
inputs GAACCCCAGCCACAGGTGGAGGTTCACATGCTATTACTATTATATGAACACCCCCCAGGTGTGGTCCCAC
       ::: :::..        :.:..:::.: :. :::: :      ::        ::::        ::
       GAATCCCGA------GAGATGGTAC-CGGGCTAGT----TT----------CCCCAT---------CAT
          470            480       490                              500

         630       640       650       660       670       680       690
inputs CCCAGTGACCCCCTGGAGATTCTGCCCTCAGGCGTGTCTAGGAAGCCCTCCCTCCTGACCCTGCAGGGCC
       : :.:::::: ::          ::::.::
       CACGGTGACCGCC----------GCCCACAG--------------------------------------
          510            520

         700       710       720       730       740       750       760     .
inputs CTGTCCTGGCCCCTGGGCAGAGCCTGACCCTCCAGTGTGGCTCTGATGTCGGCTACGACAGATTTGTTCT
                   :.::.:::.      ::.. ::                    :::::..:      ::::
       ------------------CGGAACCTA-----CCGATG---------------CTACAGC-------TTCT
                         530          540                  540           550

         770       780       790       800       810       820       830
inputs GTATAAGGAGGGGGAACGTGACTTCCTCCAGCGCCCTGGCCAGCAGCCCCAGGCTGGGCTCTCCCAGGCC
                                                   ::::::::
       ----------------------------------------CCAGCAG----------------------

         840       850       860       870       880       890       900
inputs AACTTCACCCTGGGCCCTGTGAGCCCCTCCCACGGGGGGCCAGTACAGGTGCTATGGTGCACACAACCTCT
                   ::.:::.                                                .::::
       -----------GGACCCA------------------------------------------TACCT--
                  560

         910       920       930       940       950       960       970
inputs CCTCCGAGTGGTCGGCCCCCAGCGACCCCCTGAACATCCTGATGGCAGGACAGATCTATGACACCGTCTC
                   :::::::::::::::::::::::::::.:         ::.         :.:::
       -------GTGGTCGGCCCCCAGCGACCCCCTGGA----------GCT---------TGTG----------
               570       580       590                  600

         980       990      1000      1010      1020      1030      1040
inputs CCTGTCAGCACAGCCGGGCCCCACAGTGGCCTCAGGAGAGAACGTGACCCTGCTGTGTCAGTCATGGTGG
       ::::       :.::     ::..:.::.::                 :::.::      :.::
       ---GTCA-------CAGGAACCTCTGTGACC----------------CCCAGC-----CGGT--------
                     610       620                      630

        1050      1060      1070      1080      1090      1100      1110
inputs CAGTTTGACACTTTCCTTCTGACCAAAGAAGGGGCAGCCCATCCCCCACTGCGTCTGAGATCAATGTACG
                 :.::..:.:: :              :: ::.:::                      .::
       ------------TACCAACAGAAC----------CA--CCTTCC--------------------TCG
                   640                             650

        1120      1130      1140      1150      1160      1170      1180
```

FIGURE 3b

```
inputs GAGCTCATAAGTACCAGGCTGAATTCCCCATGAGTCCTGTGACCTCAGCCCACGCGGGGACCTACAGGTG
       :..            ::.:::::: :            .:...::.:        ::: :.      ::.: .
       GTA------------GCAGAATTCTC---------AGAAGCCAC------CGCTGA-----ACTG--A
       660                    670              680              690

       1190      1200      1210      1220      1230      1240      1250
inputs CTACGGCTCATACAGCTCCAACCCCCACCTGCTGTCTTTCCCCAGTGAGCCCCTGGAACTCATGGTCTCA
       :  ::  :::::.::   :  :::       . .:::::  :  ::.  .     :::..:::    :::
       C--CGTCTCATTCA---CAAAC-------AAGTCTT--CACAA-------CTGAGACT-----TCT--
           700          710        720                            730

       1260      1270      1280      1290      1300      1310      1320
inputs GGACACTCTGGAGGCTCCAGCCTCCCACCCACAGGGCCGCCCTCCACACCTGGTCTGGGAAGATACCTGG
       .  .:::: ::   .::.::  .  :::  :::.   : :    :.:.::.:  :::
       --------AGGAGTATC--ACCACCAGTCCAAAGGA--GTCAGACTCTCCAG--CTGG------------
           740         750         760         770

       1330      1340      1350      1360      1370      1380      1390
inputs AGGTTTTGATTGGGGTCTCGGTGGCCTTCGTCCTGCTGCTCTTCCTCCTCCTCTTCCTCCTCCTCCGACG
                                       ::::::          :: ::.  :    :: :..:..: :
       ----------------------------TCCTGC----------CCGCCAGTA-----CTACACCAAGG
                                   780                   790              800

       1400      1410      1420      1430      1440      1450      1460
inputs TCAGCGTCACAGCAAACACAGGACATCTGACCAGAGAAAGACTGATTTCCAGCGTCCTGCAGGGGCTGCG
       ::.:           :.::.:          : ::::.:  :: ::    :::::::
       GCAAC-------------CTGGTC-------------CGGATAT---GCCTC-----GGGGCTG--
               810                            820              830

       1470      1480      1490      1500      1510      1520      1530
inputs GAGACAGAGCCCAAGGACAGGGGCCTGCTGAGGAGGTCCAGCCCAGCTGCTGACGTCCAGGAAGAAAACC
       .::  :: ::  .:        ::::  :  ::.: :  :.:       ::.:: :  :.::        :
       -----TGATCCTAATAA-----TCCTG--GCGGGGTTTCTG-------GCAGA-GGACTGG--------C
            840          850       860               870

       1540      1550      1560      1570      1580      1590      1600
inputs TCTATGCTGCCGTGAAGGACACACAGTCTGAGG-ACAGGGTGGAGCTGGACAGT-CAGAGCCCACACGAT
       .:          .::::: .::::  .:.:   ::: :: ::::::   ::.::.:: :::::  ::..:.
       AC-----AGCCG--GAGGAAGCGC---CTGCGGCACAGGG-----GCAGGGCTGTGCAGAGGCCGCT----
            880         890       900           910            920

       1610      1620      1630      1640      1650      1660      1670
inputs GAAGACCCCCAGGCAGTGACGTATGCCCCGGTGAAACACTCCAGTCCTAGGAGAGAAATGGCCTCTCCTC
       .::                   :::::: :                                  :: :   :
       ----TCC---------------GCCCCTG---------------------------------CCGC----C
                           930                                        940

       1680      1690      1700      1710      1720      1730      1740
inputs CCTCCTCACTGTCTGGGGAATTCCTGGACACAAAGGACAGACAGGTGGAAGAGGACAGGCAGATGGACAC
       :::::: :.:.:.:       :: :.: .::     :: :.::       ::.::::: :::::
       CCTCC--CGCAGAC---------CCGGAAATCA------CA--CGGG-------GGTCAGG---ATGGA---
            950               960                 970            980
```

FIGURE 3c

```
        1750        1760        1770        1780        1790          1800        1810
inputs  TGAGGCTGCTGCATCTGAAGCCTCCCAGGATGTGACCTACGCCCAGCTGCACAGCTTGACCCTTAGACGG
        :::         :..:        ::::::::                    ::::::             .::
        ---GGC-----CGAC-----------------AGGATGTT---------------CACAGC-----------CG-
                                        990                    1000

        1820        1830        1840        1850        1860        1870        1880
inputs  AAGGCAACTGAGCCTCCTCCATCCCAGGAAGGGGAACCTCCAGCTGAGCCCAGCATCTACGCCACTCTGG
                                   :.::... :                          .::.
        ----------------------------CGGGTTATG------------------------TTCA------------
                                   1010

        1890
inputs  CCATCCAC

        --------
```

FIGURE 3d

```
ALIGN calculates a global alignment of two sequences
 version 2.0uPlease cite: Myers and Miller, CABIOS (1989)
> hT268 a.a.                                      339 aa vs.
> GenPept U91928 - Human clone HL9 monocyte inhib    631 aa
scoring matrix: pam120.mat, gap penalties: -12/-4
23.0% identity;        Global alignment score: -647

             10        20        30        40       .50        60
inputs  MSPSPTALFCLGLCLG-RVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGPPGVDLYRLEKLSSS----
        :.:. :::.:::: :: :. .:.::.:::.: : :.:... :::..::: .. ::..: .:.
        MTPALTALLCLGLSLGPRTRVQAGPFPKPTLWAEPGSVISWGSPVTIWCQGSLEAQEYRLDKEGSPEPLD
             10        20        30        40        50        60        70

             70        80        90       100       110 . -. 120      130
inputs  RYQ-----DQAVLFIPAHKRSLAGRYRCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGDV
        : .     ..: . ::.:    ::::::: : ... :: :::.:::: :: ..::.::: :.:.:.:::..
        RJINPLEPKNKARFSIPSMTEHHAGRYRCHYYSSAGWSEPSDPLELVMTGFYNKPTLSALPSPVVASGGNM
             80        90       100       110       120       130       140

inputs  TLQCQT----------------------------------------------------RY----------------
        ::.: .                                                    :.
        TLRCGSQKGYHHFVLMKEGEHQLPRTLDSQQLHSGGFQALFPVGPVNPSHRWRFTCYYYYMNTPQVWSHP
             150       160       170       180       190       200       210

                                                    140       150
inputs  -----------------------------------------GFDQFALYKEGDP--------------------
                                                  :.:.:.:::::.
        SDPLEILPSGVSRKPSLLTLQGPVLAPGQSLTLQCGSDVGYDRFVLYKEGERDFLQRPGQQPQAGLSQAN
             220       230       240       250       260       270       280

                                                                          160
inputs  -----------APYK------------------NP-------------------------------ERW--
                    ..:.             .:                                    . :
        FTLGPVSPSHGGQYRCYGAHNLSSEWSAPSDPLNILMAGQIYDTVSLSAQPGPTVASGENVTLLCQSWWQ
             290       300       310       320       330       340       350

                                         170       180       190       200
inputs  --------------------------YRASFPIITVTAAHSGTYRCYSFSSRDPYLWSAPSDPLELVVTG
                                  :.: ::.  ::.::.::::::. : .: : : ::.::::.:.:
        FDTFLLTKEGAAHPPLRLRSHYGAHKYQAEFPHSPVTSAHAGTYRCYGSYSSNPHLLSFPSEPLELHVSG
             360       370       380       390       400       410       420

         210       220       230              240       250       260
inputs  TSVTPSRLPTEPPSS--VAEFSEATAELTVSFTNKVF--------TTETSRSITTSPKESD--SPAGPA-
        : .: :: :::. .. . :. ..:.:. .:        :. :..... .: ::!.:
        HSGGSSLPPTGPPSTPGLGRYLEVLIGVSVAFVLLLFLLLFLLLRRQRHSKHRTSDQRKTDFQRPAGAAE
             430       440       450       460       470       480       490

         270       280       290
inputs  RQYYTKGNLVRICLGAVIL-----IILAGFLAEDW---------------------HSRRKR--------
        .  .:: :  .: .        .. .::.                          :: .:
```

FIGURE 4a

```
TEPKDRGLLRRSSPAADVQEENLYAAVKDTQSEDRVELDSQSPHDEDPQAVTYAPVKHSSPRREMASPPS
         500         510         520         530         540 · ¯· 550         560

              300                              310         320              330
inputs ------LRHRGRAVQ--RPL---------------PPLPPLPQTRK------SHGGQDGGRQDVHSRGLC
         :   ..: :.  :..                   ..: .:  ::       :. :.  . ... .
      SLSGEFLDTKDRQVEEDRQMDTEAAASEASQDVTYAQLHSLTLRRKATEPPPSQEGEPPAEPSIYATLAI
         570         580         590         600         610         620         630

inputs S

       H
```

FIGURE 4b

Alignments of top-scoring domains:
ig: domain 1 of 2, from 41 to 90: score 4.1, E = 6.1

```
                *->GesvtLtCsvsgfgppgvsvtWyfkngk.lgpsllgysysrlesgek
                   + vtL+C+           + v  y +  k  ++         r++ +
     hT268    41     EKPVTLRCQGP------PGVDLY-RLEKlSSS---------RYQDQ-- 70


                 anlsegrfsissltLtissvekeDsGtYtCvv<-·
                                ++L i    +++  +G Y+C
     hT268    71  ------------AVLFIPAMKRSLAGRYRCSY      90
```

FIGURE 5A

```
ig: domain 2 of 2, from 127 to 182: score 19.1, E = 0.1
                 *->GesvtLtCsvsgfgppgvsvtWyfkngk.lgpsllgysysrlesgek
                    G++vtL+C+++    +   ++  Y k+g++ +      y+++
        hT268   127    GGDVTLQCQTR---YGFDQFALY-KEGDpAP-----YKNPERWYR-- 162

                 anlsegrfsissltLtissvekeDsGtYtCvv<-*
                    ++++i++v++   sGtY+C
        hT268   163  ------------ASFPIITVTAAHSGTYRCYS     182
```
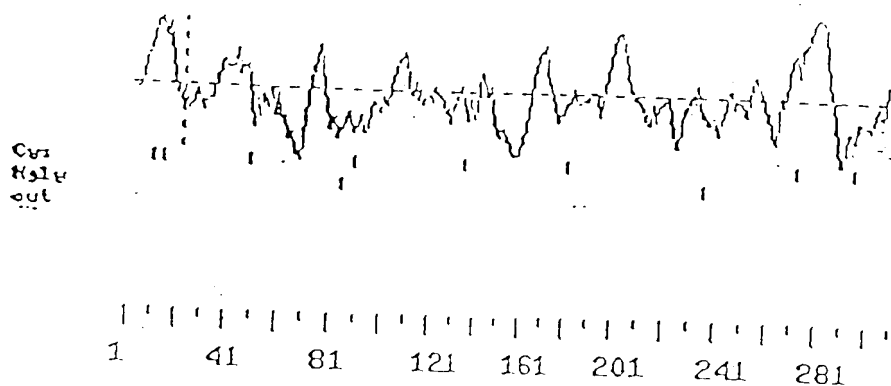
FIGURE 5B

```
                                                                      M   S   P   A     <
GAGTCGACCCACGCGTCCGCTTCCCTGCTTGGCCACATAGCTCAGGACTGGGTTGCAGAACC ATG TCT CCA GCC     74
      S   P   T   F   F   C   I   G   L   C   V   L   Q   V   I   Q   T   Q   S   G    2<
     TCA CCC ACT.TTC TTC TGT ATT GGG CTG TGT GTA CTG CAA GTG ATC CAA ACA CAG AGT GGC  13<
      P   L   P   K   P   S   L   Q   A   Q   P   S   S   L   V   P   L   G   Q   S    <<
     CCA CTC CCC AAG CCT TCC CTC CAG GCT CAG CCC AGT TCC CTG GTA CCC CTG GGT CAG TCA  19<
      V   I   L   R   C   Q   G   P   P   D   V   D   L   Y   R   L   E   K   L   K    6<
     GTT ATT CTG AGG TGC CAG GGA CCT CCA GAT GTG GAT TTA TAT CGC CTG GAG AAA CTG AAA  25<
      P   E   K   Y   E   D   Q   D   F   L   F   I   P   T   H   E   R   S   N   A    8<
     CCG GAG AAG TAT GAA GAT CAA GAC TTT CTC TTC ATT CCA ACC ATG GAA AGA AGT.AAT GCT  31<
      G   R   Y   R   C   S   Y   Q   N   G   S   H   W   S   L   P   S   D   Q   L    10<
     GGA CGG TAT CGA TGC TCT TAT CAG AAT GGG AGT CAC TGG TCT CTC CCA AGT GAC CAG CTT  37<
      E   L   I   A   T   G   V   Y   A   K   P   S   L   S   A   H   P   S   S   A    12<
     GAG CTA ATT GCT ACA GGT GTG TAT GCT AAA CCC TCA CTC TCA GCT CAT CCC AGC TCA GCA  43<
      V   P   Q   G   R   D   V   T   L   F   C   Q   S   P   Y   S   F   D   E   F    14<
     GTC CCT CAA GGC AGG GAT GTG ACT CTG AAG TGC CAG AGC CCA TAC AGT TTT GAT GAA TTC  49<
      V   L   Y   K   E   G   D   T   G   P   Y   K   R   P   E   K   W   Y   R   A    16<
     GTT CTA TAC AAA GAA GGG GAT ACT GGG CCT TAT AAG AGA CCT GAG AAA TGG TAC CGG GCC  55<
      N   F   P   I   I   T   V   T   A   A   H   S   G   T   Y   R   C   Y   S   F    18<
     AAT TTC CCC ATC ATC ACA GTG ACT GCT GCT CAC AGT GGG ACG TAC CGG TGT TAC AGC TTC  61<
      S   S   S   S   P   Y   L   W   S   A   P   S   D   P   L   V   L   V   V   T    20<
     TCC AGC TCA TCT CCA TAC CTG TGG TCA GCC CCG AGT GAC CCT CTA GTG CTT GTG GTT ACT  67<
      G   L   S   A   T   P   S   Q   V   P   T   E   E   S   F   P   V   T   E   S    22<
     GGA CTC TCT GCC ACT CCC AGC CAG GTA CCC ACG GAA GAA TCA TTT CCT GTG ACA GAA TCC  73<
      S   R   R   P   S   I   L   P   T   N   K   I   S   T   T   E   K   P   M   N    24<
     TCC AGG AGA CCT TCC ATC TTA CCC ACA AAC AAA ATA TCT ACA ACT GAA AAG CCT ATG AAT  79<
      I   T   A   S   P   E   G   L   S   P   P   I   G   F   A   H   Q   H   Y   A    26<
     ATC ACT GCC TCT CCA GAG GGG CTG AGC CCT CCA ATT GGT TTT GCT CAT CAG CAC TAT GCC  85<
      K   G   N   L   V   R   I   C   L   G   A   T   I   I   I   I   L   L   G   L    28<
     AAG GGG AAT CTG GTC CGG ATA TGC CTT GGT GCC ACG ATT ATA ATA ATT TTG TTG GGG CTT  91<
      L   A   E   D   W   H   S   R   K   K   C   L   Q   H   R   M   R   A   L   Q    30<
     CTA GCA GAG GAT TGG CAC AGT CGG AAG AAA TGC CTG CAA CAC AGG ATG AGA GCT.TTG CAA  97<
      R   P   L   P   P   L   P   L   A   *                                          31<
     AGG CCA CTA CCA CCC CTC CCA CTG GCC TAG                                          100<

AAATAACTTGGCTTTCAGCAGAGGGATTGACCAGACATCCATGCACAACCATGGACATCACCACTAGAGCCACAGACAT  1083

GGACATACTCAAGAGTGGGGAGGTTATATAAAAAAAATGAGTGTGGAGAATAAATGCAGAGCCAACAAGGTGAAAAAAA  1162

A                                                                                  1163
```

FIGURE 6

Cut
Hole
out

```
 1      41      81     121    161    201    241    281
```

MSPASPTFFCIGLCVLQVIQTQSGPLPKPSLQAQPSSLVPLGQSVILRCQGPPDVDLYRL
EKLKPEKYEDQDFLFIPTMERSNAGRYRCSYQNGSHWSLPSDQLELIATGVYAKPSLSAH
PSSAVPQGRDVTLKCQSPYSFDEFVLYKEGDTGPYKRPEKWYRANFPIITVTAAHSGTYR
CYSFSSSSPYLWSAPSDPLVLVVTGLSATPSQVPTEESFPVTESSRRPSILPTNKISTTE
KPMNITASPEGLSPPIGFAHQHYAKGNLVRICLGATIIIILLGLLAEDWHSRKKCLQHRM
RALQRPLPPLPLA

FIGURE 7

```
ALIGN calculates a global alignment of two sequences
 version 2.0uPlease cite: Myers and Miller, CABIOS (1989)
> U91928 ORF
                                          1893 aa vs.
> mT268 ORF
                                          939 aa
scoring matrix: pam120.mat, gap penalties: -12/-4
34.3% identity;        Global alignment score: -836

           10        20        30        40        50        60        70
inputs ATGACGCCCGCCCTCACAGCCCTGCTCTGCCTTGGGCTGAGTCTGGGCCCCAGGACCCGCGTGCAGGCAG
       :::.:  ::  :::  ::::   ::     .::  :::   :::::..:
       ATGTCTCCAGCC-TCAC--CC----ACTTTCTT---CTGTAT------------------------------
          10        20        30

           80        90       100       110       120       130       140
inputs GGCCCTTCCCCAAACCCACCCTCTGGGCTGAGCCAGGCTCTGTGATCAGCTGGGGGAGCCCCGTGACCAT
                       :::::::                 :::::..:.::
       -----------------------------TGGGCTG---------TGTGTACTGC-----------------
                                                   40

          150       160       170       180       190       200       210
inputs CTGGTGTCAGGGGAGCCTGGAGGCCCAGGAGTACCGACTGGATAAAGAGGGAAGCCCAGAGCCCTTGGAC
                           :.:.:..::                   ::..: :::::     :::
       ----------------------AAGTGATCC------------------AAACACAGAG----TGG--
                             50                        60        70

          220       230       240       250       260       270       280
inputs AGAAATAACCCACTGGAACCCAAGAACAAGGCCAGATTCTCCATCCCATCCATGACAGAGCACCATGCGG
           ::::::     :::     ::::       ::.::::: ::::  :
       --------CCCACT----CCC-----CAAG----------CCTTCCC-TCCAGG----------------
                80                               90

          290       300       310       320       330       340       350
inputs GGAGATACCGCTGCCACTATTACAGCTCTGCAGGCTGGTCAGAGCCCCAGCGACCCCCTGGAGCTGGTGAT
          :  :.:::                             :::. :::.: :. :::::::. :.:
       --------CTCAGCC-------------------------CAGTTCCCTG-GTACCCCTGGGTCAG-----
               100                             110       120

          360       370       380       390       400       410       420
inputs GACAGGATTCTACAACAAACCCACCCTCTCAGCCCTGCCCAGCCCTGTGGTGGCCTCAGGGGGGAATATG
       .::: :: :.:                              ::.::::: :  :::::.
       -TCAG--TTATTC---------------------------------TGAGGTG-C--CAGGGA--------
       130                                     140       150

          430       440       450       460       470       480
inputs ACCCTCC-GATGTGGCTCACAGAAGGGATATCACCATTTTGTTCTGATGAAGGAAGGAGAACACCAGCTC
       ::::: :::::::         :  :::::.::.  .  ...:::::..
       --CCTCCAGATGTGG-------ATTTATATCGCCTGGAGAAACTGAAA----------------------
         160                 170       180       190

       490       500       510       520       530       540       550
inputs CCCCGGACCCTGGACTCACAGCAGCTCCACAGTGGGGGGGTTCCAGGCCCTGTTCCCTGTGGGCCCCGTGA
       :::::     ::                  :::. :..:.:: ::.:    ::: ::         :.:
```

FIGURE 8a

```
      --CCGGA-----GA---------------AGTATGAAGATCAAGAC---TTTCTCTT------CATT-
                    200          210           220

        560      570      580      590      600      610      620
inputs ACCCCAGCCACAGGTGGAGGTTCACATGCTATTACTATTATATGAACACCCCCCAGGTGTGGTCCCACCC
       :::.::: .:...::.::.   :::::              :.:          :::.:
      ---CCAACCATGGAAAGAAGTA---ATGCT-------------GGAC--------GGTAT----------
        230      240        250                                260

        630      640      650      660      670      680      690
inputs CAGTGACCCCCTGGAGATTCTGCCCTCAGGCGTGTCTAGGAAGCCCTCCCTCCTGACCCTGCAGGGCCCT
       :..:: : ::.            ::::.      ..::.:: :               .:.:: : ::
      CGATG---CTCTTA----------TCAGA------ATGGGAGTC----------------ACTGGTCTCT
        270                   280                                 290

        700      710      720      730      740      750      760
inputs GTCCTGGCCCCTGGGCAGAGCCTGACCCTCCAGTGTGGCTCTGATGTCGGCTACGACAGATTTGTTCTGT
       :::..:            ::::: : .:.:      ::..::   :::::
      --------CCCAAG--------TGACCAGCTTGAG------CTAATT---GCTAC--------------
        300                  310           320

        770      780      790      800      810      820      830
inputs ATAAGGAGGGGGAACGTGACTTCCTCCAGCGCCCTGGCCAGCAGCCCCAGGCTGGGCTCTCCCAGGCCAA
       :::..: : ...: ..:: ::::                              .:::::
      ---AGGTGTGTATGCTAAAC--CCTC----------------------------ACTCTC---------
        330      340                                        350

        840      850      860      870      880      890      900
inputs CTTCACCCTGGGCCCTGTGAGCCCCTCCCACGGGGGCCAGTACAGGTGCTATGGTGCACACAACCTCTCC
                      ::: : :::::                     :::
      ------------------AGCTCATCCCA-----------------GCT---------------------
                         360

        910      920      930      940      950      960      970
inputs TCCGAGTGGTCGGCCCCCAGCGACCCCCTGAACATCCTGATGGCAGGACAGATCTATGACACCGTCTCCC
               :::::.. :::        ::    :-.:::::::    :::   .::::.: :.
      ----------------CAGCAGTCCC-------TC---AAGGCAGG---GAT--GTGACTCTGA-----
                       370           380         390        400

        980      990      1000     1010     1020     1030     1040
inputs TGTCAGCCACAGCCGGGCCCCACAGTGGCCTCAGGAGAGAACGTGACCCTGCTGTGTCAGTCATGGTGGCA
       .::      :::.:. :::: :                               :::: .::.::.
      AGT-------GCCAGAGCCCATA-------------------------------CAGTTTTGATGA--
                 410                                         420

       1050     1060     1070     1080     1090     1100     1110
inputs GTTTGACACTTTCCTTCTGACCAAAGAAGGGGCAGCCCATCCCCCACTGCGTCTGAGATCAATGTACGGA
       .::: :::::.. ::::::::::::     ::     :::: : :: : : :...:. : ::
      ---------ATTCGTTCTATACAAAGAAGGGG------AT-----ACTGGGCCTTATA--AGAGACCTGA
                430      440      450              460        470

       1120     1130     1140     1150     1160     1170     1180
```

FIGURE 8b

```
inputs GCTCATAAGTACCAGGCTGAATTCCCCATGAGTCCTGTGACCTCAGCCCACGCGGGGACCTACAGGTGCT
       :  :...:::::.::: .:.:.:::::::: :    :.:::::  :..:: :::.  ::::: ::: :::: :
       G--AAATGGTACCGGGCCAATTTCCCCATCATCACAGTGACTGCTGCTCACAGTGGGACGTACCGGTGTT
       480       490       500       510       520       530       540

       1190      1200      1210      1220      1230      1240      1250
inputs ACGGCTCATACAGCTCCAACCCCCACCTGCTGTCTTTCCCCAGTGAGCCCCTGGAACTCATGGTCTCAGG
       ::.:::  : ::::::: .  :: :::::  :::.   ::: :::::.: ::.:..:: .:::: .:.::
       ACAGCTTCTCCAGCTCATCTCCATACCTGTGGTCAGCCCCGAGTGACCCTCTAGTGCTTGTGGTTACTGG
       550       560       570       580       590       600       610

       1260      1270      1280      1290      1300      1310      1320
inputs ACACTCTGGAGGCTCCAGCCTCCCACCCACAGGGCCGCCCTCCACACCTGGTCTGGGAAGATACCTGGAG
       ::.:::::    :::  ::::::  ::  ::   .:::.:         ::. .:...  ..:.:::::
       ACTCTCTG------CCA--CTCCCAGCC--AGGT--ACCCAC-------GGA-AGAATCATTTCCTG---
       620             630         640              650       660

       1330      1340      1350      1360      1370      1380      1390
inputs GTTTTGATTGGGGTCTCGGTGGCCTTCGTCCTGCTGCTCTTCCTCCTCCTCTTCCTCCTCCTCCGACGTC
       :::         :.:..  :::   ::.:  .:  :::::.      ::::  :     ::: .::..
       ----TGA---------CAGAATCCT----CCAGGAGACCTTCCA-----TCTTAC----CCACAAACAAA
                       670         680               690         700

       1400      1410      1420      1430      1440      1450      1460
inputs AGCGTCACAGCAAACACAGGACATCTGACCAGAGAAAGACTGATTTCCAGCGTCCTGCAGGGGCTGCGGA
       :    :  .:..:::   :..:.:   ...:.:...::::..:   : :  ::. :  :::.: :::::::::
       A---TATCTACAA----CTGAA----AAGCCTATGAATATC--ACTGCCT-C-TCCAG-AGGGGCTG----
          710         720        730              740              750

       1470      1480      1490      1500      1510      1520      1530
inputs GACAGAGCCCAAGGACAGGGGCCTGCTGAGGAGGTCCAGCCCAGCTGCTGACGTCCAGGAAGAAAACCTC
       :::::.          ::   :. .:::   .:: :: :.::.             :
       -----AGCCCT----------CC-----AATTGGTTTTGCTCATCAGCA--------------------C
       760                 770       780                                    .

       1540      1550      1560      1570      1580      1590      1600
inputs TATGCTGCCGTGAAGGACACACAGTCTGAGGACAGGGTGGAGCTGGACAGTCAGAGCCCACACGATGAAG
       :::::                           ::.:: :.: :::::.:              ::.. ::.:
       TATGC----------------------------CAAGGGGAATCTGGTC-------------CGGATATG
       790                             800                          810

       1610      1620      1630      1640      1650      1660      1670
inputs ACCCCCAGGCAGTGACGTATGCCCCGGTGAAACACTCCAGTCCTAGGAGAGAAATGGCCTCTCCTCCCTC
        ⌐:: .::         :::: ::.:                  :: .: :....::
       ---CCTTGG---------TGCCACGAT---------------TATAATAATTTTGT-------------
          820          830                       840

       1680      1690      1700      1710      1720      1730      1740
inputs CTCACTGTCTGGGGAATTCCTGGACACAAAGGACAGACAGGTGGAAGAGGACAGGCAGATGGACACTGAG
       :::::  :::.: ::..: ::.:::::  .:.:              :::: :.::.:.:       :
       ---------TGGGGCTT--CTAG---CAGAGGATTGGC-----------ACAGTCGGAAGAA-----AT
                850         860                         870       880
```

FIGURE 8c

```
       1750        1760        1770        1780        1790        1800        1810
inputs GCTGCTGCATCTGAAGCCTCCCAGGATGTGACCTACGCCCAGCTGCACAGCTTGACCCTTAGACGGAAGG
       ::   :::::.:.              :::::::.::                    :::: .:          .:::
       GC--CTGCAACA----------CAGGATGAGA------------------GCTTTGC---------AAAGG
           890                      900                         GCTTTGC        910

       1820        1830        1840        1850        1860        1870        1880
inputs CAACTGAGCCTCCTCCATCCCAGGAAGGGGAACCTCCAGCTGAGCCCAGCATCTACGCCACTCTGGCCAT
       :  :::.      ::.:::             :::::                       :.::::::::
       CCACTA-----CCACC---------------CCTCC---------------------CACTGGCC--
       920                            930

       1890
inputs CCAC

       ----
```

FIGURE 8d

ALIGN calculates a global alignment of two sequences
version 2.0uPlease cite: Myers and Miller, CABIOS (1989)
> mT268 a.a.
                                  313 aa vs.
> GenPept U91928 - Human clone HL9 monocyte inhib   631 aa
scoring matrix: pam120.mat, gap penalties: -12/-4
20.3% identity;   Global alignment score: -802

```
                   10        20        30        40        50        60
inputs MSPASPTFFCIGLCVLQVIQTQSGPLPKPSLQAQPSSLVPLGQSVILRCQGPPDVDLYRLEKL-KPERYE
       :.::   ...:.::  .  .   ...:.::.:::.: :.:.:...  :  .:..:::.  ...  :::  ::
       MTPALTALLCLGLSLGPRTRVQAGPFPKPTLWAEPGSVISWGSPVTIWCQGSLEAQEYRLDKEGSPEPLD
           10        20        30        40        50        60        70

         70                80        90        100      110       120       130
inputs DQDFL-------F-IPTMERSNAGRYRCSYQNGSHWSLPSDQLELIATGVYAKPSLSAHPSSAVPQGRDV
       .. :        : ::.:   .::::::: :  ... :: :::.:::. :: :.::.::: ::..:.  : ..
       RNNPLEPKNKARFSIPSMTEHHAGRYRCHYYSSAGHSEPSDPLELVHTGFYNKPTLSALPSPVVASGGMM
           80        90        100      110       120       130       140

inputs TLKC--QSPY------------------------------------------------------------
       ::.:   :  :
       TLRCGSQKGYHHFVLMKEGEHQLPRTLDSQQLHSGGFQALFPVGPVNPSHRWRFTCYYYYHMTPQVWSHP
           150       160       170       180       190       200       210

                                               140       150
inputs ----------------------------------------SFDEFVLYKEGD-------------------
                                               ..: ::::::::.
       SDPLEILPSGVSRKPSLLTLQGPVLAPGQSLTLQCGSDVGYDRFVLYKEGERDFLQRPGQQPQAGLSQAN
           220       230       240       250       260       270       280

                                                                          160
inputs ----------TGPYK-----------------------------------RP-------------EKW--
                 :.:.                                      .:              . :
       FTLGPVSPSHGGQYRCYGAHNLSSEWSAPSDPLNILMAGQIYDTVSLSAQPGPTVASGENVTLLCQSWHQ
           290       300       310       320       330       340       350

                                170       180       190       200
inputs --------------------------YRANFPIITVTAAHSGTYRCYSFSSSSPYLWSAPSDPLVLVVTG
                                 :.:.::.  ::.::.:::::::.  ::..: : : ::.:: :.:.:
       FDTFLLTKEGAAHPPLRLRSMYGAHKYQAEFPHSPVTSAHAGTYRCYGSYSSNPHLLSFPSEPLELMVSG
           360       370       380       390       400       410       420

       210                    220
inputs LSATPSQVPTEES--------------FPV-----------------------------------------
       :.  .:  ::   .                : .
       HSGGSSLPPTGPPSTPGLGRYLEVLIGVSVAFVLLLFLLLFLLLRRQRHSKHRTSDQRKTDFQRPAGAAE
           430       440       450       460       470       480       490

              .            230       240       250       260       270
inputs TESS-----RRPS---------ILPTNKISTTEKPHNI-TASPEGLSP-PIGFAH--QHYAKGNLVR--I
       ::.      ::.:          .  .:  .: ... . ::  . .: .. .:  .  .. ...
```

FIGURE 9a

```
          TEPKDRGLLRRSSPAADVQEENLYAAVKDTQSEDRVELDSQSPHDEDPQAVTYAPVRHSSPRREMASPPS
               500       510       520       530       540       550       560

               280       290                 300                 310
inputs  CLGATIIIILLGLLAEDWH---------------SRKKCLQHRHRALQRPL-----PP--------LPL
          :.. .. .    ..::..              ..  : : .: . :     ::        :..
          SLSGEFLDTKDRQVEEDRQMDTEAAASEASQDVTYAQLHSLTLRRKATEPPPSQEGEPPAEPSIYATLAI
               570       580       590       600       610       620       630

inputs A.

       H
```

FIGURE 9b

```
Alignments of top-scoring domains:
ig: domain 1 of 2, from 42 to 91: score 10.2, E = 1.4
                 *->GesvtLtCsvsgfgppgvsvtWyfkngk.lgpsllgysysrlesgek
                    G+sv L+C+           ++v  y +  k ++         +++e +
     mT268    42    GQSVILRCQGP------PDVDLY-RLERIKP--------EKYEDQ-- 71

                 anlsegrfsissltLtissvekeDsGtYtCvv<-*
                                L i + e++++G Y+C
     mT268    72 ------------DFLFIPTHERSNAGRYRCSY        91
```

FIGURE 10A

```
ig: domain 2 of 2, from 128 to 183: score 9.6, E = 1.6
               *->GesvtLtCsvsgfgppgvsvthyfkngk.lgpsllgysysrlesgek
                  G +vtL C++          ++  y k+g++ +         y+r+e    +
   mT268   128    GRDVTLKCQSP---YSFDEFVLY-KEGDtGP-------YKRPEKW-Y 162


               anlsegrfsissltLtissvekeDsGtYtCvv<-*
               +   .             ++i++v++  sGtY+C
   mT268   163 RA-----------NFPIITVTAAHSGTYRCYS      183
```

FIGURE 10B

ALIGN calculates a global alignment of two sequences
 version 2.0uPlease cite: Myers and Miller, CABIOS (1989)
 > hT268 a.a.   339 aa vs.
 > mT268 a.a.   313 aa
scoring matrix: pam120.mat, gap penalties: -12/-4
64.4% identity;   Global alignment score: 1011

```
           10        20        30        40        50        60
inputs HSPSPTALFCLGLCLGRV-PAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGPPGVDLYRLEKLSSSRYQD
       :::.. ..::.::::. .: ..::::::::::::: :::::::: ...::::::::.:::::::: . .::
       HSPASPTFFCIGLCVLQVIQIQSGPLPKPSLQAQPSSLVPLGQSVILRCQGPPDVDLYRLEKLKPEKYED
           10        20        30        40        50        60        70

        70        80        90        100       110       120       130
inputs QAVLFIPAVKPSLAGRYRCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLQCQTRYG
       :. :::::.: :: :::::::::::: :::::::::::.::::.:::::::::.:..::. : :::::.::. :.
       QDFLFIPTHERSNAGRYRCSYQNGSHWSLPSDQLELIATGVYAKPSLSAHPSSAVPQGRDVTLKCQSPYS
        80        90        100       110       120       130       140

       140       150       160       170       180       190       200
inputs FDQFALYKEGDPAPYKNPERWYRASFPIITVTAAHSGTYRCYSFSSRDPYLWSAPSDPLELVVTGTSVTP
       ::.:.:::::.:::. :::::::::::::::::::::::::::::: .::::::::::: ::::: :.::
       FDEFVLYKEGDTGPYKRPEKWYRANFPIITVTAAHSGTYRCYSFSSSSPYLWSAPSDPLVLVVTGLSATP
       150       160       170       180       190       200       210

       210       220       230       240       250       260       270
inputs SRLPTEPPSSVAEFSEATAELTVSFTNKVFTTETSRSITTSPKESDSPAGPARQYYTKGNLVRICLGAVI
       :..::: . .:.: . : :::. ::: . .::.:: ..: : :.: :.:::::::::.:
       SQVPTEESFPVTESSRRPSILP---TNKISTTEKPHNITASPEGLSPPIGFAHQHYAKGNLVRICLGATI
       220       230       240       250       260       270

       280       290       300       310       320       330
inputs LIILAGFLAEDWHSRRKRLRHRGRAVQRPLPPLPPLPQTRKSHGGQDGGRQDVHSRGLCS
       .::: :.:::::::::.: :.:: ::.::::::::: :.
       IIILLGLLAEDWHSRKKCLQHRHRALQRPLPPLP-LA------------------------
       280       290       300       310
```

FIGURE 11
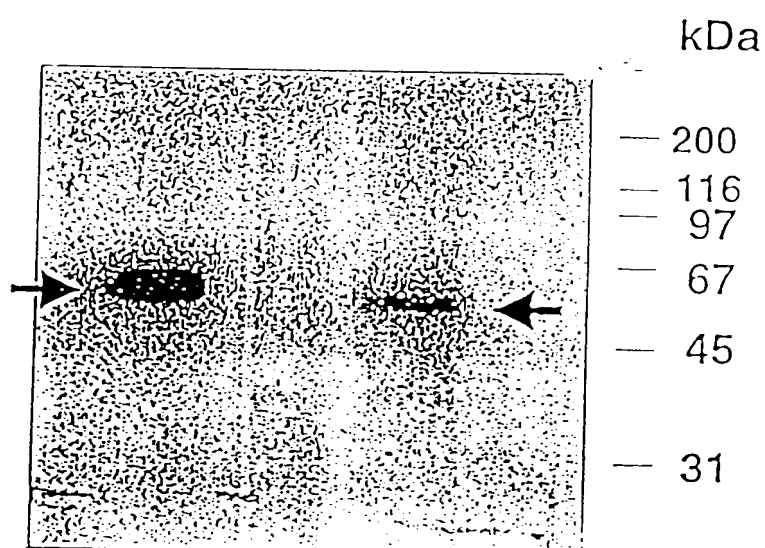
FIGURE 12
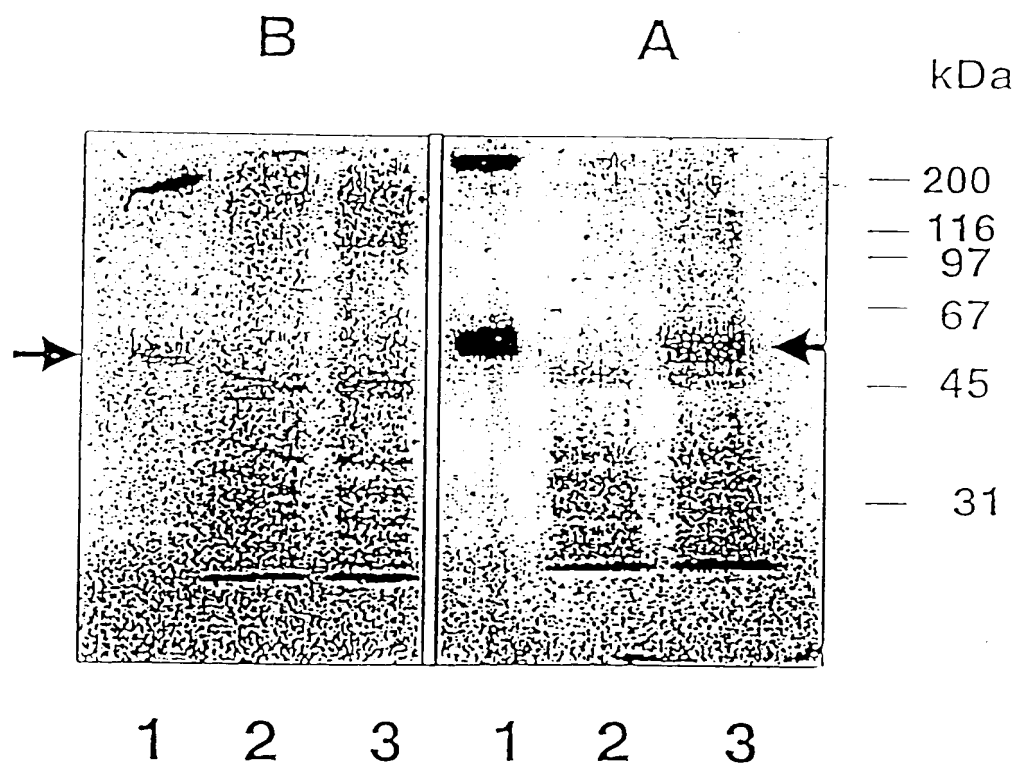
FIGURE 13
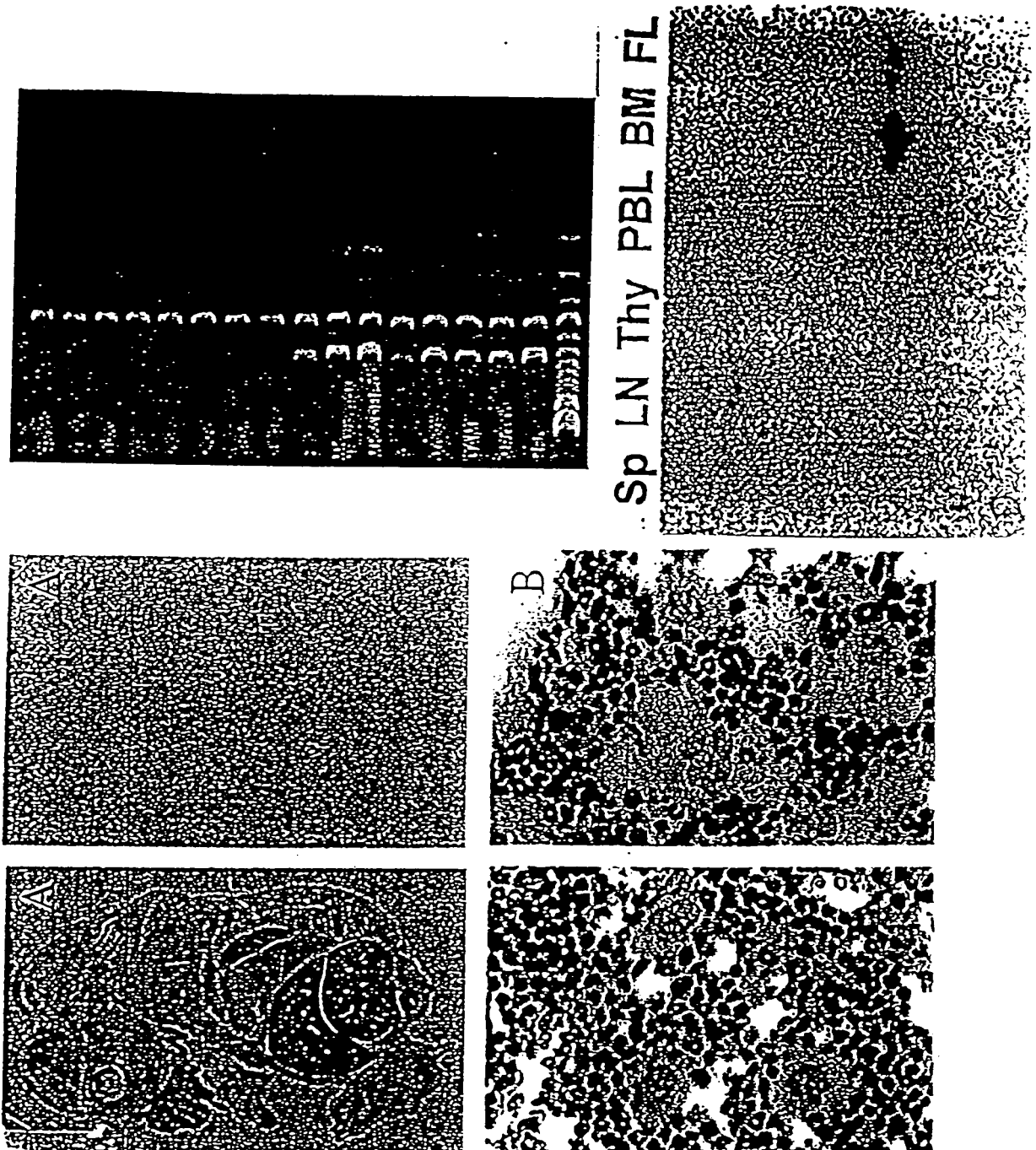
FIGURE 14

FIGURE 15

Adhesion %
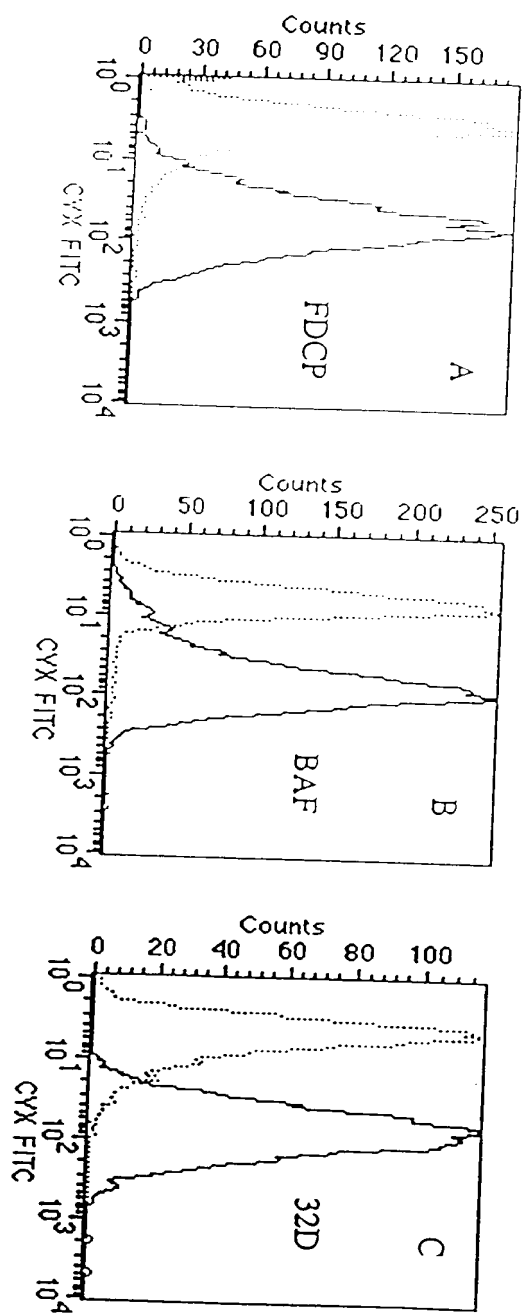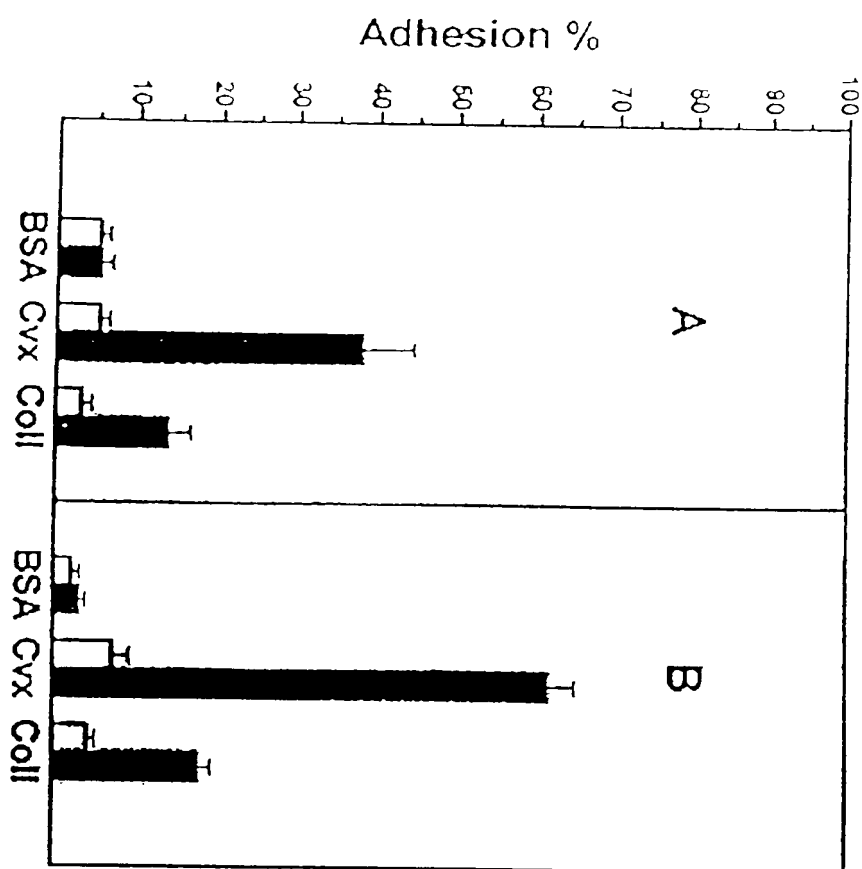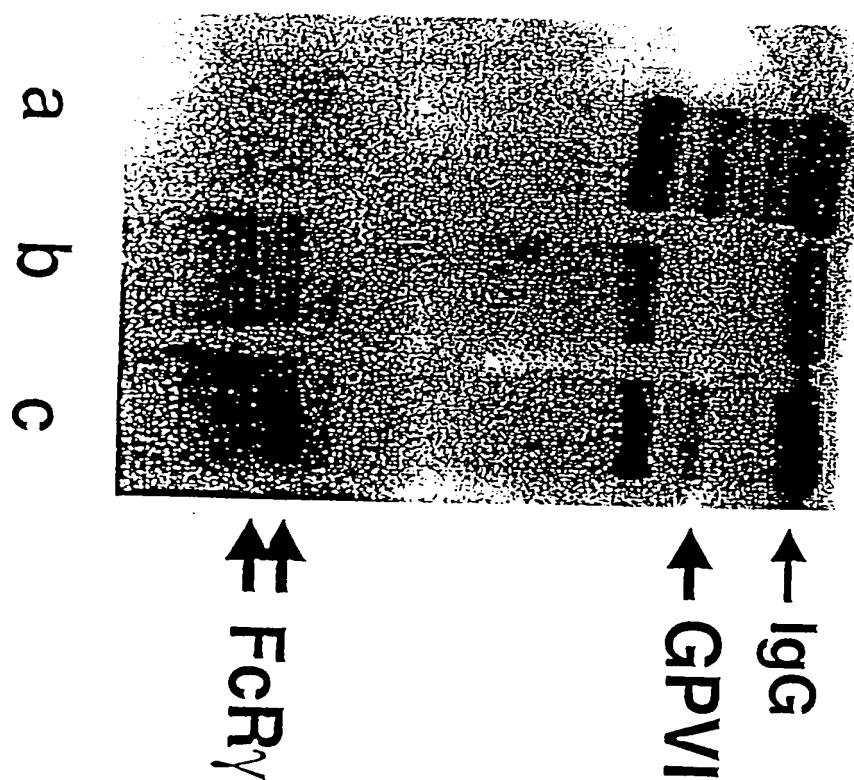
FIGURE 16

FIGURE 17

FIGURE 18

FIGURE 19

Bleeding time (seconds)

Retroviruses

ms

268fl

268ex

Effets des monoclonaux sur la liaison GPVI-Fc/coll type I

FIGURE 20

Effet des monoclonaux sur la liaison
GPⅥ-Fc / Convulxine
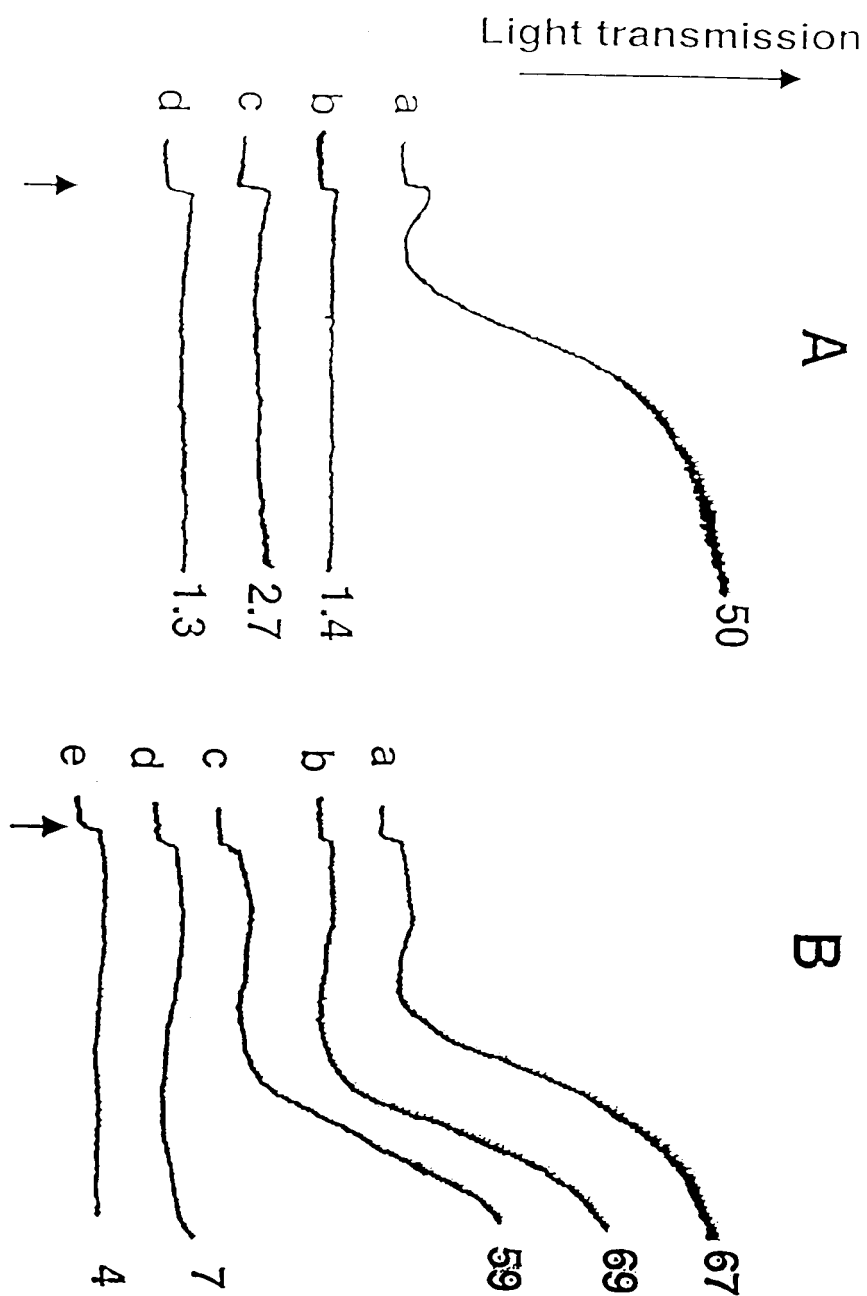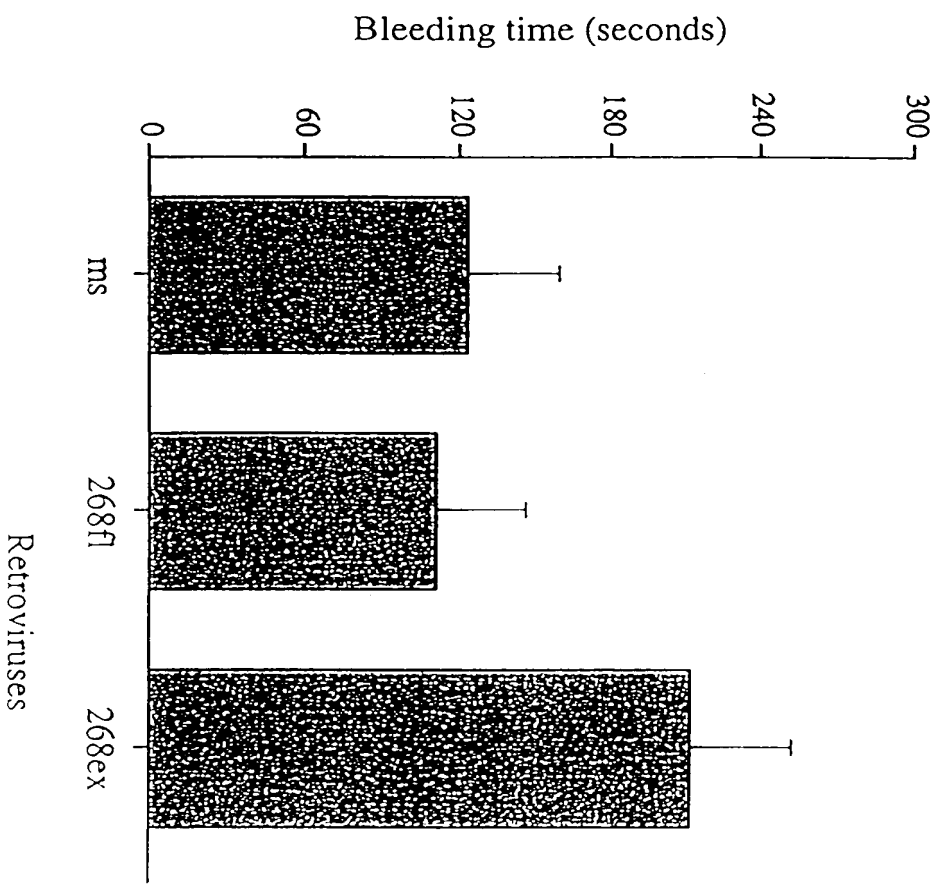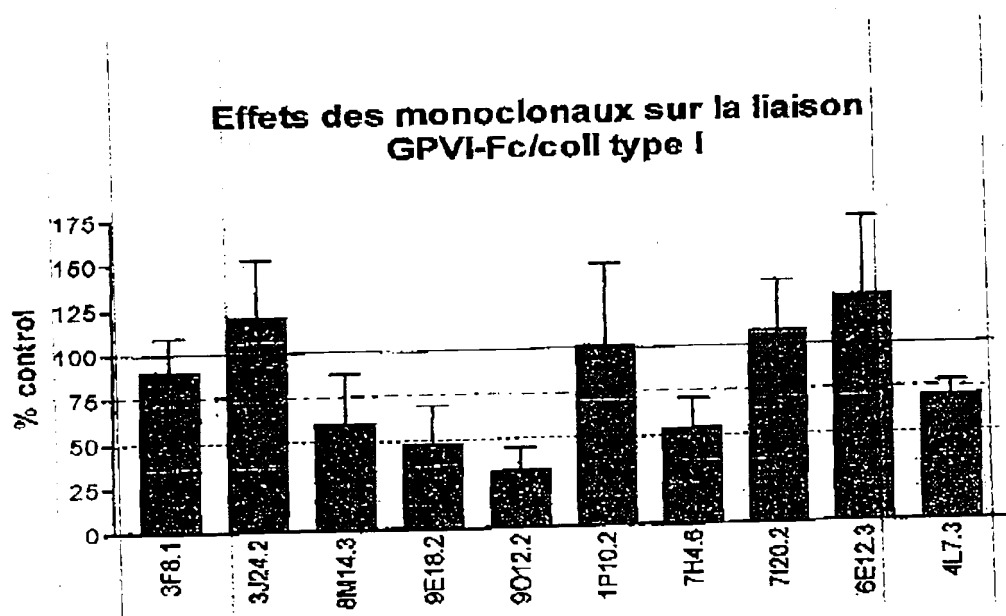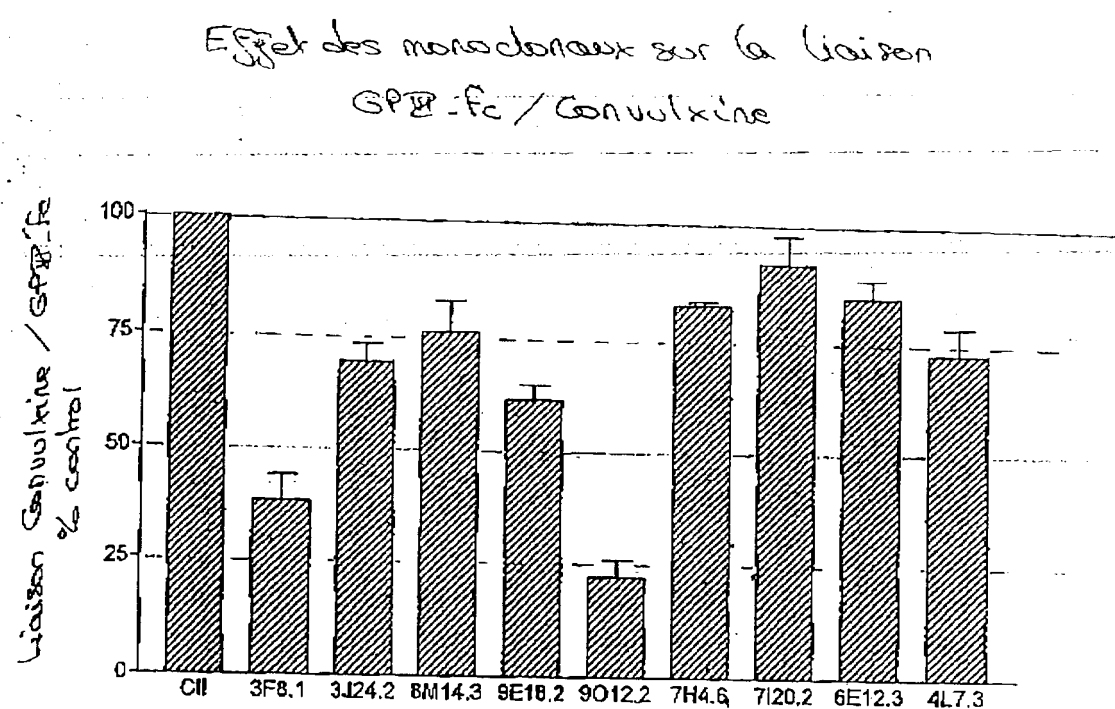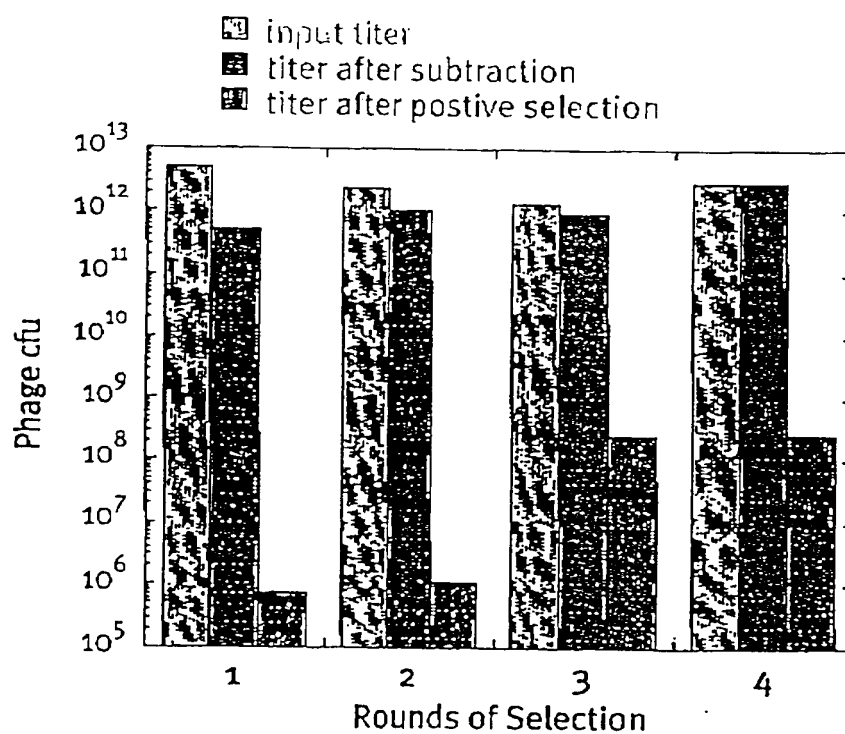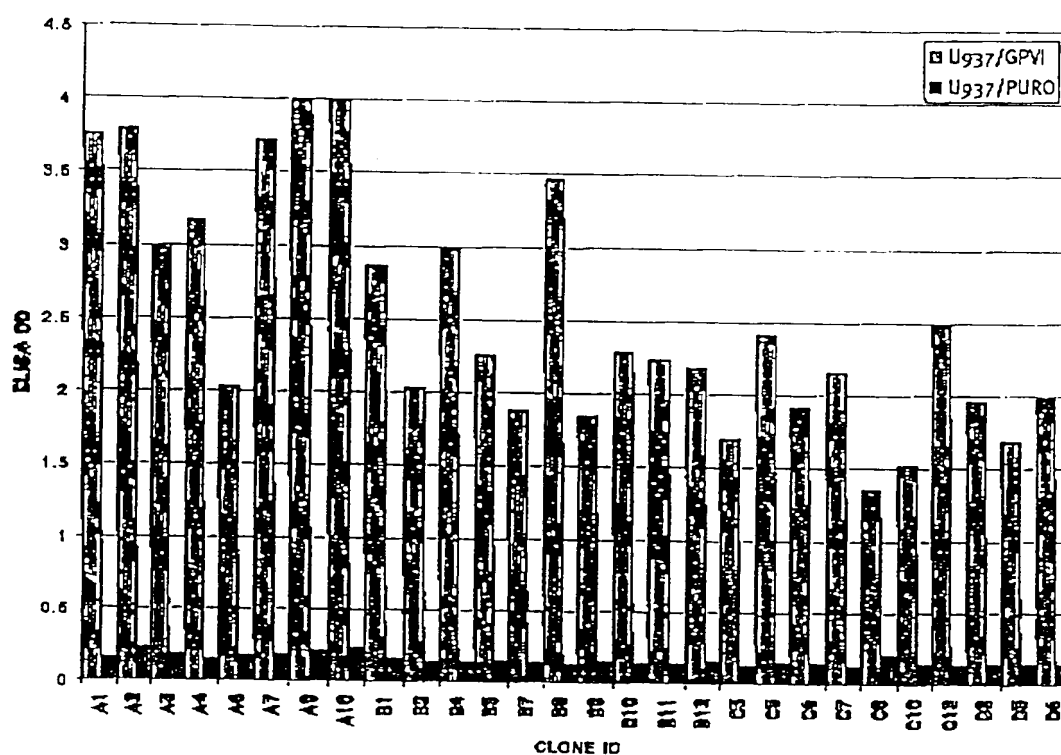
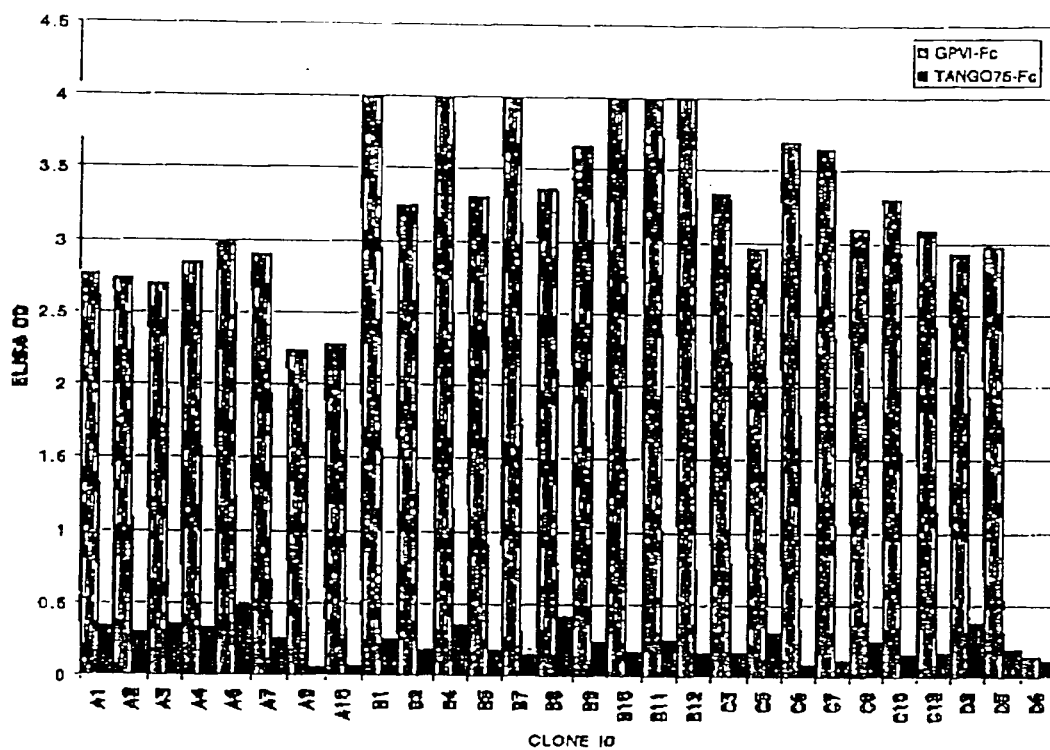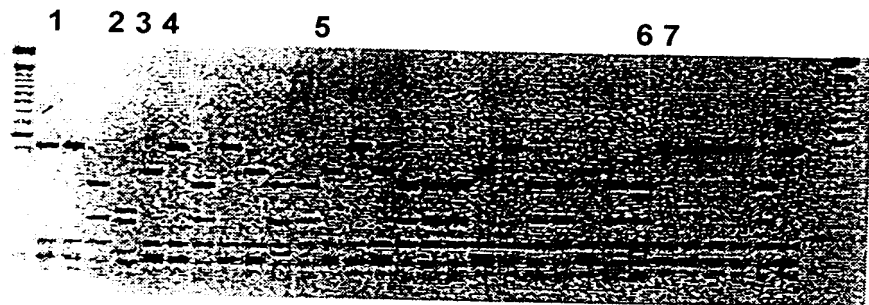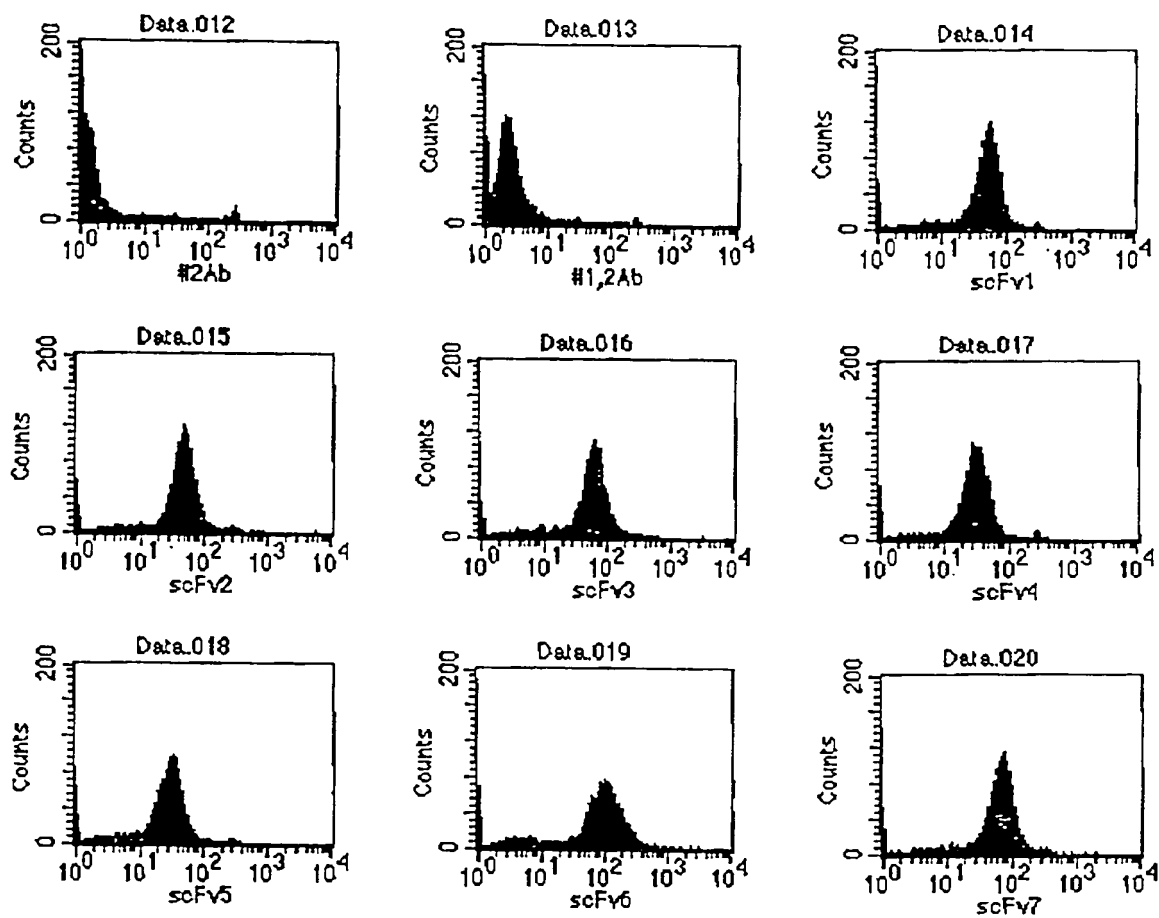**FIGURE 21**

FIGURE 22

FIGURE 23a

FIGURE 23b

FIGURE 24

scFv1:A4
scFv2:B4
scFv3:A9
scFv4:C3
scFv5:C9
scFv6:C10
scFv7:A10

FIGURE 25

FIGURE 26

FIGURE 27